

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/582,393  
Source: IFWP  
Date Processed by STIC: 6/19/06

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)**
- 2. U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER:

10/582,393

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2      Invalid Line Length     The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
  
- 4 ✓ Non-ASCII     The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
  
- 5      Variable Length     Sequence(s)      contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)           . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
  
- 7      Skipped Sequences  
    (OLD RULES)     Sequence(s)      missing. If intentional, please insert the following lines for **each** skipped sequence:  
                               (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                               (i)       SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                               (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                               This sequence is intentionally skipped  
                               Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
  
- 8      Skipped Sequences  
    (NEW RULES)     Sequence(s)      missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
                               <210> sequence id number  
                               <400> sequence id number  
                               000
  
- 9      Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                               Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                               In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
  
- 10      Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
  
- 11      Use of <220>     Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
  
- 12      PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13      Misuse of n/Xaa     "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWP

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/582,393

DATE: 06/19/2006  
TIME: 12:26:14

Input Set : A:\PTO.KD.txt  
SEQUENCE LISTING Output Set: N:\CRF4\06192006\J582393.raw

W--> 1 SEQUENZPROTOKOLL  
3 <110> APPLICANT: Greiner Bio-One  
5 <120> TITLE OF INVENTION: Sonden zum Nachweis genitaler HPV-Genotypen  
7 <130> FILE REFERENCE: 25974  
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/582,393  
C--> 10 <141> CURRENT FILING DATE: 2006-06-09  
12 <160> NUMBER OF SEQ ID NOS: 135  
14 <170> SOFTWARE: PatentIn Ver. 2.1

use English for a U.S. application

see item 4 on  
Err summary  
sheet

## ERRORED SEQUENCES

16 <210> SEQ ID NO: 1  
17 <211> LENGTH: 25  
18 <212> TYPE: DNA Human  
19 <213> ORGANISM: Humanes Papilloma-Virus  
21 <400> SEQUENCE: 1  
E--> 22 cargcnaaw wwktdaarga ytggt 25  
25 <210> SEQ ID NO: 2  
26 <211> LENGTH: 25 Human  
27 <212> TYPE: DNA  
28 <213> ORGANISM: Humanes Papilloma-Virus  
30 <400> SEQUENCE: 2  
E--> 31 cargcnaaat atktraaaga ttgtg 25  
1222 <210> SEQ ID NO: 135  
1223 <211> LENGTH: 26 Human  
1224 <212> TYPE: DNA  
1225 <213> ORGANISM: Humanes Papilloma-Virus  
1227 <400> SEQUENCE: 135  
1228 taattagatt ttgcaaggg tgcgtt 26  
E--> 1238 -1- delete at end of file

This "messy" occurs in all sequences

Does Not Comply  
Corrected Diskette Needed

see p.2  
for error  
explanation

see p. 2

VARIABLE LOCATION SUMMARY

DATE: 06/19/2006

PATENT APPLICATION: US/10/582,393

TIME: 12:26:15

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\06192006\J582393.raw

*error explanation!*

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:1; N Pos. 6

Seq#:2; N Pos. 6

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/582,393

DATE: 06/19/2006

TIME: 12:26:15

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\06192006\J582393.raw

L:1 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:  
L:9 M:270 C: Current Application Number differs, Replaced Application Number  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:22 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1  
L:31 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2  
L:1238 M:254 E: No. of Bases conflict, this line has no nucleotides.